Amendments to the Specification:

Please replace the paragraph beginning at page 9, line 12, with the following:

--Figure 2 is a diagram showing a base sequence (SEQ ID NO:1) of about 8 Kb of a DNA fragment including the PEPC gene.--

Please replace the paragraph beginning at page 9, line 15, with the following:

--Figure 3 is a continuation of Figure 2 (SEQ ID NO:1).--

Please replace the paragraph beginning at page 9, line 17, with the following:

--Figure 4 is a continuation of Figure 3 (SEQ ID NO:1).--

Please replace the paragraph beginning at page 20, line 8, with the following:

--A maize PEPC genome gene was isolated by a method described in the literature (Eur. J. Biochem. 181: 593-598, 1989). Maize (Zea mays L. cv. Golden Cross Bantam) was planted in vermiculite. The planted maize was cultured in a culture chamber in darkness at 30°C for 4 days. Genome DNA was isolated from etiolated leaves in accordance with a method of Matsuoka et al., Plant Physiol. 85: 942-946 (1985). This genome DNA was digested with XbaI and fractionated by 10% to 40% sucrose density gradient centrifugation. The obtained XbaI fragment was ligated to the XbaI arms of the phage λong C (Stratagene, CA) and the ligated DNA was packaged in vitro. The genomic library was constructed using the packaged DNA. Then, the phage plaques were screened by plaque hybridization using as a probe the sequence 5'-GTCCACGAGAAGATCCAGGG-3' (SEQ ID NO:2) described in Matsuoka et al., Plant Cell Physiol. 30: 479-486 (1989). cDNA clone (pPEP3055) isolated by using this probe

Appl. No. 10/714,054
Amdt. dated March 17, 2004
Reply to Notice to Comply of February 17, 2004

PATENT

can also be used as a probe. A positive clone was isolated, and the nucleotide sequence of the genomic clone was determined by a dideoxy method. About 8 Kb of XbaI-XbaI fragment containing the full-length PEPC structural gene was obtained. Figure 1 shows a restriction map of a DNA fragment containing the obtained PEPC, and Figures 2 through 4 show the nucleotide sequence thereof (SEQ ID NO:1).--

· Please replace the paragraph (Table 1) beginning at page 21, line 5, with the following:

--Table 1

Element	Position		Sequence	SEQ ID NO:
TATA box	-24 to -28		TATTT	-
CCAAT box	-367 to -371		CCAAT	-
Sp-1 binding site	-80 to -85		CCGCCC	-
	-48 to -53		CCGCCC	-
	275 to 280	(intron 1)	CCGCCG	-
	281 to 286	(intron 1)	CCGCCC	-
Light responsive element	-653 to -661		CCTTATCCT	-
Direct repeat	-536 to -550		CCCTCAACCACATCCTGC	3
sequence	-510 to -527		GACGCCCTCG-CCACATCC	4
	-453 to -470		GACGCCCTCT-CCACATCCTGC	5
	-378 to -395		GACGCCCTCT-CCACATCCTGC	5
	-201 to -214		CCCTCT-CCACATCC	6
	-30 to -39		CT-CCACATCC	7

--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 6, at the end of the application.